ABSTRACT OF THE DISCLOSURE

The invention relates to protein-protein interactions and methods for identifying interacting proteins and the amino acid sequence at the site of interaction. Using overlapping hexapeptides that encode for the entire amino acid sequences of the linker domains of human P-glycoprotein gene 1 and 3 (HP-gp1 and HP-gp3), a direct and specific binding between P-gp1 and 3 linker domains and intracellular proteins was demonstrated. Three different stretches (^{617}EKGIYFKLVTM^{627}, ^{658}SRSSLIRKRSTRRSVRGSQA^{677} and ^{694}PVSFWRIMKLNLT^{706} for P-gp1 and ^{618}LMKKEGVYFKLVNM^{631}, ^{648}KAATRMAPNGWKSRLFRHSTQKNLKNS^{674} and ^{695}PVSFLKVLKLNKT^{677} for P-gp3) in linker domains bound to proteins with apparent molecular masses of ~80 kDa, 57 kDa and 30 kDa. The binding of the 57 kDa protein was further characterized. Purification and partial N-terminal amino acid sequencing of the 57 kDa protein showed that it encodes the N-terminal amino acids of alpha and beta-tubulins. The method of the present invention was further validated with Annexin. The present invention thus demonstrates a novel concept whereby the interactions between two proteins are mediated by strings of few amino acids with high and repulsive binding energies, enabling the identification of high-affinity binding sites between any interacting proteins.